

30	35	40	45	
aac ttc gat ccg atc gac aag aat cag atc cag ctg ttc aat ctg gaa	Asn Phe Asp Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu	195		
50	55	60		
tct tcc aaa atc gaa gtt atc ctg aag aat gct atc gta tac aac tct	Ser Ser Lys Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser	243		
65	70	75		
atg tac gaa aac ttc tcc acc tcc ttc tgg atc cgt atc ccg aaa tac	Met Tyr Glu Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr	291		
80	85	90		
ttc aac tcc atc tct ctg aac aat gaa tac acc atc atc aac tgc atg	Phe Asn Ser Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met	339		
95	100	105		
gaa aac aat tct ggt tgg aaa gta tct ctg aac tac ggt gaa atc atc	Glu Asn Asn Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile	387		
110	115	120	125	
tgg act ctg cag gac act cag gaa atc aaa cag cgt gtt gta ttc aaa	Trp Thr Leu Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys	435		
130	135	140		
tac tct cag atg atc aac atc tct gac tac atc aat cgc tgg atc ttc	Tyr Ser Gln Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe	483		
145	150	155		
gtt acc atc acc aac aat cgt ctg aat aac tcc aaa atc tac atc aac	Val Thr Ile Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn	531		
160	165	170		
ggc cgt ctg atc gac cag aaa ccg atc tcc aat ctg ggt aac atc cac	Gly Arg Leu Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His	579		
175	180	185		
gct tct aat aac atc atg ttc aaa ctg gac ggt tgt cgt gac act cac	Ala Ser Asn Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His	627		
190	195	200	205	
cgc tac atc tgg atc aaa tac ttc aat ctg ttc gac aaa gaa ctg aac	Arg Tyr Ile Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn	675		
210	215	220		
gaa aaa gaa atc aaa gac ctg tac gac aac cag tcc aat tct ggt atc	Glu Lys Glu Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile	723		
225	230	235		
ctg aaa gac ttc tgg ggt gac tac ctg cag tac gac aaa ccg tac tac	Leu Lys Asp Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr	771		
240	245	250		
atg ctg aat ctg tac gat ccg aac aaa tac gtt gac gtc aac aat gta	Met Leu Asn Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val	819		
255	260	265		
ggg atc cgc ggt tac atg tac ctg aaa ggt ccg cgt ggt tct gtt atg	Gly Ile Arg Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met	867		
270	275	280	285	

act acc aac atc tac ctg aac tct tcc ctg tac cgt ggt acc aaa ttc	915
Thr Thr Asn Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe	
290 295 300	
atc atc aag aaa tac gcg tct ggt aac aag gac aat atc gtt cgc aac	963
Ile Ile Lys Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn	
305 310 315	
aat gat cgt gta tac atc aat gtt gta gtt aag aac aaa gaa tac cgt	1011
Asn Asp Arg Val Tyr Ile Asn Val Val Lys Asn Lys Glu Tyr Arg	
320 325 330	
ctg gct acc aat gct tct cag gct ggt gta gaa aag atc ttg tct gct	1059
Leu Ala Thr Asn Ala Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala	
335 340 345	
ctg gaa atc ccg gac gtt ggt aat ctg tct cag gta gtt gta atg aaa	1107
Leu Glu Ile Pro Asp Val Gly Asn Leu Ser Gln Val Val Val Met Lys	
350 355 360 365	
tcc aag aac gac cag ggt atc act aac aaa tgc aaa atg aat ctg cag	1155
Ser Lys Asn Asp Gln Gly Ile Thr Asn Lys Cys Lys Met Asn Leu Gln	
370 375 380	
gac aac aat ggt aac gat atc ggt ttc atc ggt ttc cac cag ttc aac	1203
Asp Asn Asn Gly Asn Asp Ile Gly Phe Ile Gly Phe His Gln Phe Asn	
385 390 395	
aat atc gct aaa ctg gtt gct tcc aac tgg tac aat cgt cag atc gaa	1251
Asn Ile Ala Lys Leu Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu	
400 405 410	
cgt tcc tct cgc act ctg ggt tgc tct tgg gag ttc atc ccg gtt gat	1299
Arg Ser Ser Arg Thr Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp	
415 420 425	
gac ggt tgg ggt gaa cgt ccg ctg taa gaattc	1332
Asp Gly Trp Gly Glu Arg Pro Leu *	
430 435	

<210> 2
 <211> 437
 <212> PRT
 <213> Synthetic Construct

<220>

<400> 2

Met Arg Leu Leu Ser Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile Asn	
1 5 10 15	
Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu	
20 25 30	
Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp	
35 40 45	
Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys	
50 55 60	
Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu	
65 70 75 80	

Asn	Phe	Ser	Thr	Ser	Phe	Trp	Ile	Arg	Ile	Pro	Lys	Tyr	Phe	Asn	Ser		
				85					90					95			
Ile	Ser	Leu	Asn	Asn	Glu	Tyr	Thr	Ile	Ile	Asn	Cys	Met	Glu	Asn	Asn		
			100					105					110				
Ser	Gly	Trp	Lys	Val	Ser	Leu	Asn	Tyr	Gly	Glu	Ile	Ile	Trp	Thr	Leu		
		115					120					125					
Gln	Asp	Thr	Gln	Glu	Ile	Lys	Gln	Arg	Val	Val	Phe	Lys	Tyr	Ser	Gln		
	130					135					140						
Met	Ile	Asn	Ile	Ser	Asp	Tyr	Ile	Asn	Arg	Trp	Ile	Phe	Val	Thr	Ile		
145				150						155				160			
Thr	Asn	Asn	Arg	Leu	Asn	Asn	Ser	Lys	Ile	Tyr	Ile	Asn	Gly	Arg	Leu		
				165				170						175			
Ile	Asp	Gln	Lys	Pro	Ile	Ser	Asn	Leu	Gly	Asn	Ile	His	Ala	Ser	Asn		
		180					185						190				
Asn	Ile	Met	Phe	Lys	Leu	Asp	Gly	Cys	Arg	Asp	Thr	His	Arg	Tyr	Ile		
	195						200					205					
Trp	Ile	Lys	Tyr	Phe	Asn	Leu	Phe	Asp	Lys	Glu	Leu	Asn	Glu	Lys	Glu		
	210				215					220							
Ile	Lys	Asp	Leu	Tyr	Asp	Asn	Gln	Ser	Asn	Ser	Gly	Ile	Leu	Lys	Asp		
225				230						235				240			
Phe	Trp	Gly	Asp	Tyr	Leu	Gln	Tyr	Asp	Lys	Pro	Tyr	Tyr	Met	Leu	Asn		
			245					250					255				
Leu	Tyr	Asp	Pro	Asn	Lys	Tyr	Val	Asp	Val	Asn	Asn	Val	Gly	Ile	Arg		
		260					265						270				
Gly	Tyr	Met	Tyr	Leu	Lys	Gly	Pro	Arg	Gly	Ser	Val	Met	Thr	Thr	Asn		
	275					280						285					
Ile	Tyr	Leu	Asn	Ser	Ser	Leu	Tyr	Arg	Gly	Thr	Lys	Phe	Ile	Ile	Lys		
	290					295					300						
Lys	Tyr	Ala	Ser	Gly	Asn	Lys	Asp	Asn	Ile	Val	Arg	Asn	Asn	Asp	Arg		
305				310						315				320			
Val	Tyr	Ile	Asn	Val	Val	Val	Lys	Asn	Lys	Glu	Tyr	Arg	Leu	Ala	Thr		
			325					330					335				
Asn	Ala	Ser	Gln	Ala	Gly	Val	Glu	Lys	Ile	Leu	Ser	Ala	Leu	Glu	Ile		
	340						345						350				
Pro	Asp	Val	Gly	Asn	Leu	Ser	Gln	Val	Val	Val	Met	Lys	Ser	Lys	Asn		
	355						360					365					
Asp	Gln	Gly	Ile	Thr	Asn	Lys	Cys	Lys	Met	Asn	Leu	Gln	Asp	Asn	Asn		
	370				375					380							
Gly	Asn	Asp	Ile	Gly	Phe	Ile	Gly	Phe	His	Gln	Phe	Asn	Asn	Ile	Ala		
385				390						395				400			
Lys	Leu	Val	Ala	Ser	Asn	Trp	Tyr	Asn	Arg	Gln	Ile	Glu	Arg	Ser	Ser		
			405					410					415				
Arg	Thr	Leu	Gly	Cys	Ser	Trp	Glu	Phe	Ile	Pro	Val	Asp	Asp	Gly	Trp		
		420					425						430				
Gly	Glu	Arg	Pro	Leu													
	435																

<210> 3
 <211> 1323
 <212> DNA
 <213> Synthetic Construct

 <220>

 <221> CDS
 <222> (13)...(1314)
 <223> Synthetic Construct

 <400> 3

Phe	Trp	Gly	Asp	Tyr	Leu	Gln	Tyr	Asp	Lys	Pro	Tyr	Tyr	Met	Leu	Asn		
		240					245					250					
ctg	tac	gat	ccg	aac	aaa	tac	gtt	gac	gtc	aac	aat	gta	ggg	atc	cgc	819	
Leu	Tyr	Asp	Pro	Asn	Lys	Tyr	Val	Asp	Val	Asn	Asn	Val	Gly	Ile	Arg		
		255				260					265						
ggg	tac	atg	tac	ctg	aaa	ggg	ccg	cgt	ggg	tct	gtt	atg	act	acc	aac	867	
Gly	Tyr	Met	Tyr	Leu	Lys	Gly	Pro	Arg	Gly	Ser	Val	Met	Thr	Thr	Asn		
		270			275					280					285		
atc	tac	ctg	aac	tct	tcc	ctg	tac	cgt	ggg	acc	aaa	ttc	atc	atc	aag	915	
Ile	Tyr	Leu	Asn	Ser	Ser	Leu	Tyr	Arg	Gly	Thr	Lys	Phe	Ile	Ile	Lys		
				290					295					300			
aaa	tac	gcg	tct	ggg	aac	aag	gac	aat	atc	gtt	cgc	aac	aat	gat	cgt	963	
Lys	Tyr	Ala	Ser	Gly	Asn	Lys	Asp	Asn	Ile	Val	Arg	Asn	Asn	Asp	Arg		
			305				310						315				
gta	tac	atc	aat	gtt	gta	gtt	aag	aac	aaa	gaa	tac	cgt	ctg	gct	acc	1011	
Val	Tyr	Ile	Asn	Val	Val	Val	Lys	Asn	Lys	Glu	Tyr	Arg	Leu	Ala	Thr		
		320					325					330					
aat	gct	tct	cag	gct	ggg	gta	gaa	aag	atc	ttg	tct	gct	ctg	gaa	atc	1059	
Asn	Ala	Ser	Gln	Ala	Gly	Val	Glu	Lys	Ile	Leu	Ser	Ala	Leu	Glu	Ile		
		335				340					345						
ccg	gac	gtt	ggg	aat	ctg	tct	cag	gta	gtt	gta	atg	aaa	tcc	aag	aac	1107	
Pro	Asp	Val	Gly	Asn	Leu	Ser	Gln	Val	Val	Val	Met	Lys	Ser	Lys	Asn		
		350			355					360					365		
gac	cag	ggg	atc	act	aac	aaa	tgc	aaa	atg	aat	ctg	cag	gac	aac	aat	1155	
Asp	Gln	Gly	Ile	Thr	Asn	Lys	Cys	Lys	Met	Asn	Leu	Gln	Asp	Asn	Asn		
				370					375					380			
ggg	aac	gat	atc	ggg	ttc	atc	ggg	ttc	cac	cag	ttc	aac	aat	atc	gct	1203	
Gly	Asn	Asp	Ile	Gly	Phe	Ile	Gly	Phe	His	Gln	Phe	Asn	Asn	Ile	Ala		
			385					390					395				
aaa	ctg	gtt	gct	tcc	aac	tgg	tac	aat	cgt	cag	atc	gaa	cgt	tcc	tct	1251	
Lys	Leu	Val	Ala	Ser	Asn	Trp	Tyr	Asn	Arg	Gln	Ile	Glu	Arg	Ser	Ser		
		400					405					410					
cgc	act	ctg	ggg	tgc	tct	tgg	gag	ttc	atc	ccg	gtt	gat	gac	ggg	tgg	1299	
Arg	Thr	Leu	Gly	Cys	Ser	Trp	Glu	Phe	Ile	Pro	Val	Asp	Asp	Gly	Trp		
		415				420					425						
ggg	gaa	cgt	ccg	ctg	taagaattc											1323	
Gly	Glu	Arg	Pro	Leu													
		430															

<210> 4

<211> 434

<212> PRT

<213> Synthetic Construct

<220>

<400> 4

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<213> Synthetic Construct

<220>

<221> CDS

<222> (13)...(1317)

<400> 5

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      Met Ala Ser Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile
          1              5              10

aat acc tcc atc ctg aac ctg cgc tac gaa tcc aat cac ctg atc gac 99
Asn Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp
      15              20              25

ctg tct cgc tac gct tcc aaa atc aac atc ggt tct aaa gtt aac ttc 147
Leu Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe
      30              35              40              45

gat ccg atc gac aag aat cag atc cag ctg ttc aat ctg gaa tct tcc 195
Asp Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser
          50              55              60

aaa atc gaa gtt atc ctg aag aat gct atc gta tac aac tct atg tac 243
Lys Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr
          65              70              75

gaa aac ttc tcc acc tcc ttc tgg atc cgt atc ccg aaa tac ttc aac 291
Glu Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn
          80              85              90

tcc atc tct ctg aac aat gaa tac acc atc atc aac tgc atg gaa aac 339
Ser Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn
          95              100              105

aat tct ggt tgg aaa gta tct ctg aac tac ggt gaa atc atc tgg act 387
Asn Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr
      110              115              120              125

ctg cag gac act cag gaa atc aaa cag cgt gtt gta ttc aaa tac tct 435
Leu Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser
          130              135              140

cag atg atc aac atc tct gac tac atc aat cgc tgg atc ttc gtt acc 483
Gln Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr
          145              150              155

atc acc aac aat cgt ctg aat aac tcc aaa atc tac atc aac ggc cgt 531
Ile Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg
          160              165              170

ctg atc gac cag aaa ccg atc tcc aat ctg ggt aac atc cac gct tct 579
Leu Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser
          175              180              185

aat aac atc atg ttc aaa ctg gac ggt tgt cgt gac act cac cgc tac 627
Asn Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr
      190              195              200              205
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<210> 6
 <211> 435
 <212> PRT
 <213> Synthetic Construct
 <220>

<400> 6
 Met Ala Ser Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile Asn Thr Ser
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 Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu Ser Arg
 20 25 30
 Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp Pro Ile
 35 40 45
 Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys Ile Glu
 50 55 60
 Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe
 65 70 75 80
 Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser
 85 90 95
 Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn Ser Gly
 100 105 110
 Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp
 115 120 125
 Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met Ile
 130 135 140
 Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn
 145 150 155 160
 Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp
 165 170 175
 Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn Asn Ile
 180 185 190
 Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile Trp Ile
 195 200 205
 Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu Ile Lys
 210 215 220
 Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp Phe Trp
 225 230 235 240
 Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn Leu Tyr
 245 250 255
 Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg Gly Tyr
 260 265 270
 Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn Ile Tyr
 275 280 285
 Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys Lys Tyr
 290 295 300
 Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg Val Tyr
 305 310 315 320
 Ile Asn Val Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr Asn Ala
 325 330 335
 Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp
 340 345 350
 Val Gly Asn Leu Ser Gln Val Val Met Lys Ser Lys Asn Asp Gln
 355 360 365
 Gly Ile Thr Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn
 370 375 380
 Asp Ile Gly Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala Lys Leu
 385 390 395 400
 Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser Arg Thr
 405 410 415

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130							135							140							
aac	gag	gac	tcc	gag	cag	tcc	atc	aac	ttc	tcc	tac	gac	atc	tcc	aac	483					
Asn	Glu	Asp	Ser	Glu	Gln	Ser	Ile	Asn	Phe	Ser	Tyr	Asp	Ile	Ser	Asn						
		145					150					155									
aac	gct	cct	ggt	tac	aac	aag	tgg	ttc	ttc	gtc	acc	gtc	acc	aac	aac	531					
Asn	Ala	Pro	Gly	Tyr	Asn	Lys	Trp	Phe	Phe	Val	Thr	Val	Thr	Asn	Asn						
		160				165					170										
atg	atg	ggt	aac	atg	aag	atc	tac	atc	aac	ggt	aag	ctg	atc	gac	acc	579					
Met	Met	Gly	Asn	Met	Lys	Ile	Tyr	Ile	Asn	Gly	Lys	Leu	Ile	Asp	Thr						
		175			180					185					190						
atc	aag	gtc	aag	gag	ttg	acc	ggt	atc	aac	ttc	tcc	aag	acc	atc	acc	627					
Ile	Lys	Val	Lys	Glu	Leu	Thr	Gly	Ile	Asn	Phe	Ser	Lys	Thr	Ile	Thr						
				195					200					205							
ttc	gag	atc	aac	aag	atc	cca	gac	acc	ggt	ctg	atc	acc	tcc	gac	tcc	675					
Phe	Glu	Ile	Asn	Lys	Ile	Pro	Asp	Thr	Gly	Leu	Ile	Thr	Ser	Asp	Ser						
			210					215					220								
gac	aac	atc	aac	atg	tgg	atc	cgt	gac	ttc	tac	atc	ttc	gcc	aag	gag	723					
Asp	Asn	Ile	Asn	Met	Trp	Ile	Arg	Asp	Phe	Tyr	Ile	Phe	Ala	Lys	Glu						
		225					230					235									
ttg	gac	ggt	aag	gac	atc	aac	atc	ctg	ttc	aac	tcc	ttg	cag	tac	acc	771					
Leu	Asp	Gly	Lys	Asp	Ile	Asn	Ile	Leu	Phe	Asn	Ser	Leu	Gln	Tyr	Thr						
	240					245					250										
aac	gtc	gtc	aag	gac	tac	tgg	ggt	aac	gac	ctg	aga	tac	aac	aag	gag	819					
Asn	Val	Val	Lys	Asp	Tyr	Trp	Gly	Asn	Asp	Leu	Arg	Tyr	Asn	Lys	Glu						
	255				260					265					270						
tac	tac	atg	gtc	aac	atc	gac	tac	ttg	aac	aga	tac	atg	tac	gcc	aac	867					
Tyr	Tyr	Met	Val	Asn	Ile	Asp	Tyr	Leu	Asn	Arg	Tyr	Met	Tyr	Ala	Asn						
				275					280					285							
tcc	aga	cag	atc	gtc	ttc	aac	acc	aga	cgt	aac	aac	aac	gac	ttc	aac	915					
Ser	Arg	Gln	Ile	Val	Phe	Asn	Thr	Arg	Arg	Asn	Asn	Asn	Asp	Phe	Asn						
			290					295					300								
gag	ggt	tac	aag	atc	atc	atc	aag	cgt	atc	aga	ggt	aac	acc	aac	gac	963					
Glu	Gly	Tyr	Lys	Ile	Ile	Ile	Lys	Arg	Ile	Arg	Gly	Asn	Thr	Asn	Asp						
		305					310					315									
acc	aga	gtc	aga	ggt	ggt	gac	atc	ctg	tac	ttc	gac	atg	act	atc	aac	1011					
Thr	Arg	Val	Arg	Gly	Gly	Asp	Ile	Leu	Tyr	Phe	Asp	Met	Thr	Ile	Asn						
		320				325					330										
aac	aag	gcc	tac	aac	ctg	ttc	atg	aag	aac	gag	acc	atg	tac	gcc	gac	1059					
Asn	Lys	Ala	Tyr	Asn	Leu	Phe	Met	Lys	Asn	Glu	Thr	Met	Tyr	Ala	Asp						
	335				340					345					350						
aac	cac	tcc	acc	gag	gac	atc	tac	gcc	atc	ggt	ctg	cgt	gag	cag	acc	1107					
Asn	His	Ser	Thr	Glu	Asp	Ile	Tyr	Ala	Ile	Gly	Leu	Arg	Glu	Gln	Thr						
				355				360						365							
aag	gac	atc	aac	gac	aac	atc	atc	ttc	cag	atc	cag	cca	atg	aac	aac	1155					
Lys	Asp	Ile	Asn	Asp	Asn	Ile	Ile	Phe	Gln	Ile	Gln	Pro	Met	Asn	Asn						
			370					375					380								

act tac tac tac gct tcc cag atc ttc aag tcc aac ttc aac ggt gag	1203
Thr Tyr Tyr Tyr Ala Ser Gln Ile Phe Lys Ser Asn Phe Asn Gly Glu	
385 390 395	
aac atc tcc ggt atc tgt tcc atc ggt acc tac aga ttc cgt ctg ggt	1251
Asn Ile Ser Gly Ile Cys Ser Ile Gly Thr Tyr Arg Phe Arg Leu Gly	
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Gly Asp Trp Tyr Arg His Asn Tyr Leu Val Pro Thr Val Lys Gln Gly	
415 420 425 430	
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Leu	Ser	Leu	Gln	Asn	Arg	Lys	Asn	Thr	Leu	Val	Asp	Thr	Ser	Gly	Tyr				
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Pro	Phe	Asp	Phe	Lys	Leu	Gly	Ser	Ser	Gly	Glu	Asp	Arg	Gly	Lys	Val				
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Ile	Val	Thr	Gln	Asn	Glu	Asn	Ile	Val	Tyr	Asn	Ser	Met	Tyr	Glu	Ser				
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Phe	Ser	Ile	Ser	Phe	Trp	Ile	Arg	Ile	Asn	Lys	Trp	Val	Ser	Asn	Leu				
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Pro	Gly	Tyr	Thr	Ile	Ile	Asp	Ser	Val	Lys	Asn	Asn	Ser	Gly	Trp	Ser				
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Ile	Gly	Ile	Ile	Ser	Asn	Phe	Leu	Val	Phe	Thr	Leu	Lys	Gln	Asn	Glu				
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Asp	Ser	Glu	Gln	Ser	Ile	Asn	Phe	Ser	Tyr	Asp	Ile	Ser	Asn	Asn	Ala				
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Pro	Gly	Tyr	Asn	Lys	Trp	Phe	Phe	Val	Thr	Val	Thr	Asn	Asn	Met	Met				
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Ile	Asn	Lys	Ile	Pro	Asp	Thr	Gly	Leu	Ile	Thr	Ser	Asp	Ser	Asp	Asn				
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Ile	Asn	Met	Trp	Ile	Arg	Asp	Phe	Tyr	Ile	Phe	Ala	Lys	Glu	Leu	Asp				
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aaa Lys	att Ile	tta Leu	att Ile	tcc Ser 35	tac Tyr	ttc Phe	aac Asn	aag Lys	ttc Phe	ttc Phe	aag Lys	aga Arg	att Ile	aag Lys 45	tct Ser	147
tct Ser	tcc Ser	gtt Val	tta Leu 50	aac Asn	atg Met	aga Arg	tac Tyr	aag Lys 55	aat Asn	gat Asp	aaa Lys	tac Tyr	gtc Val 60	gac Asp	act Thr	195
tcc Ser	ggg Gly	tac Tyr 65	gac Asp	tcc Ser	aat Asn	atc Ile	aac Asn 70	att Ile	aac Asn	ggg Gly	gac Asp	gtg Val 75	tac Tyr	aag Lys	tac Tyr	243
cca Pro	act Thr 80	aac Asn	aaa Lys	aac Asn	caa Gln	ttc Phe 85	ggg Gly	atc Ile	tac Tyr	aac Asn	gac Asp 90	aag Lys	ctt Leu	tcc Ser	gag Glu	291
gtc Val 95	aac Asn	atc Ile	tct Ser	caa Gln	aac Asn 100	gac Asp	tac Tyr	att Ile	atc Ile	tac Tyr 105	gac Asp	aac Asn	aag Lys	tac Tyr	aag Lys 110	339
aac Asn	ttc Phe	tct Ser	att Ile	tct Ser 115	ttc Phe	tgg Trp	gtc Val	agg Arg	att Ile 120	cct Pro	aac Asn	tac Tyr	gac Asp	aac Asn 125	aag Lys	387
atc Ile	gtc Val	aac Asn	gtt Val 130	aac Asn	aac Asn	gag Glu	tac Tyr	act Thr 135	atc Ile	atc Ile	aac Asn	tgt Cys	atg Met	aga Arg	gac Asp	435
aac Asn	aac Asn	tcc Ser 145	ggg Gly	tgg Trp	aag Lys	gtc Val	tct Ser 150	ctt Leu	aac Asn	cac His	aac Asn	gag Glu 155	atc Ile	att Ile	tgg Trp	483
acc Thr	ttg Leu 160	caa Gln	gac Asp	aac Asn	gca Ala	ggg Gly 165	att Ile	aac Asn	caa Gln	aag Lys	tta Leu 170	gca Ala	ttc Phe	aac Asn	tac Tyr	531
ggg Gly 175	aac Asn	gca Ala	aac Asn	ggg Gly	att Ile 180	tct Ser	gac Asp	tac Tyr	atc Ile	aac Asn 185	aag Lys	tgg Trp	att Ile	ttc Phe	gtc Val 190	579
act Thr	atc Ile	act Thr	aac Asn	gac Asp 195	aga Arg	tta Leu	ggg Gly	gac Asp	tct Ser 200	aag Lys	ctt Leu	tac Tyr	att Ile	aac Asn 205	ggg Gly	627
aac Asn	tta Leu	atc Ile	gac Asp 210	caa Gln	aag Lys	tcc Ser	att Ile	tta Leu 215	aac Asn	tta Leu	ggg Gly	aac Asn	att Ile 220	cac His	gtt Val	675
tct Ser	gac Asp	aac Asn	atc Ile	tta Leu	ttc Phe	aag Lys	atc Ile	gtt Val	aac Asn	tgc Cys	agt Ser	tac Tyr 235	acc Thr	aga Arg	tac Tyr	723
att Ile	ggc Gly 240	att Ile	aga Arg	tac Tyr	ttc Phe	aac Asn 245	att Ile	ttc Phe	gac Asp	aag Lys	gag Glu 250	tta Leu	gac Asp	gag Glu	acc Thr	771
gag Glu 255	att Ile	caa Gln	act Thr	tta Leu	tac Tyr 260	agc Ser	aac Asn	gaa Glu	cct Pro	aac Asn 265	acc Thr	aat Asn	att Ile	ttg Leu	aag Lys 270	819
gac	ttc	tgg	ggg	aac	tac	ttg	ctt	tac	gac	aag	gaa	tac	tac	tta	tta	867

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<223> Synthetic Construct

<221> CDS

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aag ctg tac aag aag atc aag gac aac tcc atc ttg gac atg aga tac 99
Lys Leu Tyr Lys Lys Ile Lys Asp Asn Ser Ile Leu Asp Met Arg Tyr
  15             20             25             30

gaa aac aat aag ttc atc gac atc tcc ggt tac ggt tcc aac atc tcc 147
Glu Asn Asn Lys Phe Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser
          35             40             45

atc aac ggt gac gtc tac atc tac tcc acc aat aga aac cag ttc gga 195
Ile Asn Gly Asp Val Tyr Ile Tyr Ser Thr Asn Arg Asn Gln Phe Gly
          50             55             60

atc tac tcc tcc aag cct tcc gag gtc aac atc gct cag aac aac gac 243
Ile Tyr Ser Ser Lys Pro Ser Glu Val Asn Ile Ala Gln Asn Asn Asp
          65             70             75

atc atc tac aac gga aga tac cag aac ttc tcc atc tcc ttc tgg gtc 291
Ile Ile Tyr Asn Gly Arg Tyr Gln Asn Phe Ser Ile Ser Phe Trp Val
      80             85             90

cgt atc cca aag tac ttc aac aag gtc aac ctg aat aac gag tac acc 339
Arg Ile Pro Lys Tyr Phe Asn Lys Val Asn Leu Asn Asn Glu Tyr Thr
  95             100             105             110

atc atc gac tgc atc cgt aac aat aac tcc gga tgg aag atc tcc ctg 387
Ile Ile Asp Cys Ile Arg Asn Asn Asn Ser Gly Trp Lys Ile Ser Leu
          115             120             125

aac tac aac aag atc atc tgg acc ctg cag gac acc gcc ggt aac aat 435
Asn Tyr Asn Lys Ile Ile Trp Thr Leu Gln Asp Thr Ala Gly Asn Asn
          130             135             140

cag aag ttg gtc ttc aac tac acc cag atg atc tcc atc tcc gac tac 483
Gln Lys Leu Val Phe Asn Tyr Thr Gln Met Ile Ser Ile Ser Asp Tyr
          145             150             155

atc aac aag tgg atc ttc gtc acc atc acc aat aac cgt ttg gga aac 531
Ile Asn Lys Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Gly Asn
          160             165             170

tcc aga atc tac atc aac ggt aac ttg atc gac gag aag tcc atc tcc 579
Ser Arg Ile Tyr Ile Asn Gly Asn Leu Ile Asp Glu Lys Ser Ile Ser
          175             180             185             190

aac ttg ggt gac atc cac gtc tcc gac aac att ttg ttc aag atc gtc 627
Asn Leu Gly Asp Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile Val
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ggt tgt aac gac acc cgt tac gtc ggg atc cgt tac ttc aaa gtc ttc 675
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Asp	Thr	Glu	Leu	Gly	Lys	Thr	Glu	Ile	Glu	Thr	Leu	Tyr	Ser	Asp	Glu		
		225					230					235					
cct	gac	cca	tcc	atc	ctg	aag	gac	ttc	tgg	ggg	aac	tac	ctg	ctg	tac	771	
Pro	Asp	Pro	Ser	Ile	Leu	Lys	Asp	Phe	Trp	Gly	Asn	Tyr	Leu	Leu	Tyr		
	240					245					250						
aac	aaa	cgt	tac	tac	ttg	ctg	aac	ttg	ttg	cgt	acc	gac	aag	tcc	atc	819	
Asn	Lys	Arg	Tyr	Tyr	Leu	Leu	Asn	Leu	Leu	Arg	Thr	Asp	Lys	Ser	Ile		
255					260					265					270		
acc	cag	aac	tcc	aac	ttc	ttg	aac	atc	aac	cag	cag	aga	ggg	gtc	tac	867	
Thr	Gln	Asn	Ser	Asn	Phe	Leu	Asn	Ile	Asn	Gln	Gln	Arg	Gly	Val	Tyr		
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Gln	Lys	Pro	Asn	Ile	Phe	Ser	Asn	Thr	Arg	Leu	Tyr	Thr	Gly	Val	Glu		
			290					295					300				
gtc	att	atc	aga	aag	aac	gga	tct	act	gat	att	tcc	aac	acc	gat	aac	963	
Val	Ile	Ile	Arg	Lys	Asn	Gly	Ser	Thr	Asp	Ile	Ser	Asn	Thr	Asp	Asn		
		305				310						315					
ttc	gtc	aga	aag	aac	gat	ctg	gct	tac	atc	aac	gtt	gtc	gac	aga	gat	1011	
Phe	Val	Arg	Lys	Asn	Asp	Leu	Ala	Tyr	Ile	Asn	Val	Val	Asp	Arg	Asp		
	320					325					330						
gtc	gaa	tac	cgt	ctg	tac	gcc	gat	atc	tct	atc	gcc	aaa	cct	gaa	aag	1059	
Val	Glu	Tyr	Arg	Leu	Tyr	Ala	Asp	Ile	Ser	Ile	Ala	Lys	Pro	Glu	Lys		
335				340						345				350			
atc	atc	aag	ctg	atc	cgt	acc	tct	aac	tct	aac	aac	tct	ctg	gga	caa	1107	
Ile	Ile	Lys	Leu	Ile	Arg	Thr	Ser	Asn	Ser	Asn	Asn	Ser	Leu	Gly	Gln		
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Ile	Ile	Val	Met	Asp	Ser	Ile	Gly	Asn	Asn	Cys	Thr	Met	Asn	Phe	Gln		
			370					375					380				
aac	aac	aac	ggg	gga	aac	atc	ggg	ttg	ttg	ggg	ttc	cac	tcc	aac	aac	1203	
Asn	Asn	Asn	Gly	Gly	Asn	Ile	Gly	Leu	Leu	Gly	Phe	His	Ser	Asn	Asn		
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Leu	Val	Ala	Ser	Ser	Trp	Tyr	Tyr	Asn	Asn	Ile	Arg	Lys	Asn	Thr	Ser		
	400					405					410						
tcc	aac	ggg	tgc	ttc	tgg	tcc	ttc	atc	tcc	aag	gag	cac	ggg	tgg	cag	1299	
Ser	Asn	Gly	Cys	Phe	Trp	Ser	Phe	Ile	Ser	Lys	Glu	His	Gly	Trp	Gln		
415					420					425					430		
gag	aac	taataggaat	tc													1317	
Glu	Asn																

[illegible]

<223> Synthetic Construct

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Tyr	Lys	Lys	Ile	Lys	Asp	Asn	Ser	Ile	Leu	Asp	Met	Arg	Tyr	Glu	Asn
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Asn	Lys	Phe	Ile	Asp	Ile	Ser	Gly	Tyr	Gly	Ser	Asn	Ile	Ser	Ile	Asn
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Gly	Asp	Val	Tyr	Ile	Tyr	Ser	Thr	Asn	Arg	Asn	Gln	Phe	Gly	Ile	Tyr
	50					55					60				
Ser	Ser	Lys	Pro	Ser	Glu	Val	Asn	Ile	Ala	Gln	Asn	Asn	Asp	Ile	Ile
65					70					75					80
Tyr	Asn	Gly	Arg	Tyr	Gln	Asn	Phe	Ser	Ile	Ser	Phe	Trp	Val	Arg	Ile
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Pro	Lys	Tyr	Phe	Asn	Lys	Val	Asn	Leu	Asn	Asn	Glu	Tyr	Thr	Ile	Ile
			100					105					110		
Asp	Cys	Ile	Arg	Asn	Asn	Asn	Ser	Gly	Trp	Lys	Ile	Ser	Leu	Asn	Tyr
		115					120					125			
Asn	Lys	Ile	Ile	Trp	Thr	Leu	Gln	Asp	Thr	Ala	Gly	Asn	Asn	Gln	Lys
	130					135					140				
Leu	Val	Phe	Asn	Tyr	Thr	Gln	Met	Ile	Ser	Ile	Ser	Asp	Tyr	Ile	Asn
145					150					155					160
Lys	Trp	Ile	Phe	Val	Thr	Ile	Thr	Asn	Asn	Arg	Leu	Gly	Asn	Ser	Arg
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Ile	Tyr	Ile	Asn	Gly	Asn	Leu	Ile	Asp	Glu	Lys	Ser	Ile	Ser	Asn	Leu
			180					185						190	
Gly	Asp	Ile	His	Val	Ser	Asp	Asn	Ile	Leu	Phe	Lys	Ile	Val	Gly	Cys
		195					200					205			
Asn	Asp	Thr	Arg	Tyr	Val	Gly	Ile	Arg	Tyr	Phe	Lys	Val	Phe	Asp	Thr
	210					215					220				
Glu	Leu	Gly	Lys	Thr	Glu	Ile	Glu	Thr	Leu	Tyr	Ser	Asp	Glu	Pro	Asp
225					230					235					240
Pro	Ser	Ile	Leu	Lys	Asp	Phe	Trp	Gly	Asn	Tyr	Leu	Leu	Tyr	Asn	Lys
			245						250					255	
Arg	Tyr	Tyr	Leu	Leu	Asn	Leu	Leu	Arg	Thr	Asp	Lys	Ser	Ile	Thr	Gln
			260					265						270	
Asn	Ser	Asn	Phe	Leu	Asn	Ile	Asn	Gln	Gln	Arg	Gly	Val	Tyr	Gln	Lys
		275					280					285			
Pro	Asn	Ile	Phe	Ser	Asn	Thr	Arg	Leu	Tyr	Thr	Gly	Val	Glu	Val	Ile
	290					295					300				
Ile	Arg	Lys	Asn	Gly	Ser	Thr	Asp	Ile	Ser	Asn	Thr	Asp	Asn	Phe	Val
305					310					315					320
Arg	Lys	Asn	Asp	Leu	Ala	Tyr	Ile	Asn	Val	Val	Asp	Arg	Asp	Val	Glu
			325						330					335	
Tyr	Arg	Leu	Tyr	Ala	Asp	Ile	Ser	Ile	Ala	Lys	Pro	Glu	Lys	Ile	Ile
			340					345						350	
Lys	Leu	Ile	Arg												

430

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<400> 17
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          Met Lys Asp Thr Ile Leu Ile Gln Val Phe Asn Asn Tyr Ile
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tcc	aac	atc	tcc	tcc	aac	gcc	atc	ctg	tcc	ctg	tcc	tac	cgt	ggg	ggg	99
Ser	Asn	Ile	Ser	Ser	Asn	Ala	Ile	Leu	Ser	Leu	Ser	Tyr	Arg	Gly	Gly	
15					20					25					30	

cgt ctg atc gac tcc tcc ggt tac gga gcc acc atg aac gtc ggt tcc 147
Arg Leu Ile Asp Ser Ser Gly Tyr Gly Ala Thr Met Asn Val Gly Ser
35 40 45

gac gtc atc ttc aac gac atc ggt aac ggt cag ttc aag ctg aac aac 195
Asp Val Ile Phe Asn Asp Ile Gly Asn Gly Gln Phe Lys Leu Asn Asn
50 55 60

tcc gag aac tcc aac atc acc gcc cac cag tcc aag ttc gtc gtc tac 243
Ser Glu Asn Ser Asn Ile Thr Ala His Gln Ser Lys Phe Val Val Tyr
65 70 75

gac tcc atg ttc gac aac ttc tcc atc aac ttc tgg gtc cgt acc cca 291
Asp Ser Met Phe Asp Asn Phe Ser Ile Asn Phe Trp Val Arg Thr Pro
80 85 90

aag tac aac aac aac gac atc cag acc tac ctg cag aac gag tac acc 339
Lys Tyr Asn Asn Asn Asp Ile Gln Thr Tyr Leu Gln Asn Glu Tyr Thr
95 100 105 110

atc atc tcc tgt atc aag aac gac tcc ggt tgg aag gtc tcc atc aag 387
Ile Ile Ser Cys Ile Lys Asn Asp Ser Gly Trp Lys Val Ser Ile Lys
115 120 125

gga aac cgt atc atc tgg acc ctg atc gac gtc aac gcc aag tcc aag 435
Gly Asn Arg Ile Ile Trp Thr Leu Ile Asp Val Asn Ala Lys Ser Lys
130 135 140

tcc atc ttc ttc gag tac tcc atc aag gac aac atc tcc gac tac atc 483
Ser Ile Phe Phe Glu Tyr Ser Ile Lys Asp Asn Ile Ser Asp Tyr Ile
145 150 155

aac aag tgg ttc tcc atc acc atc acc aac gac cgt ctg ggt aac gcc 531
 Asn Lys Trp Phe Ser Ile Thr Ile Thr Asn Asp Arg Leu Gly Asn Ala
 160 165 170

aac atc tac atc aac ggt tcc ctg aag aag tcc gag aag atc ctg aac 579
Asn Ile Tyr Ile Asn Gly Ser Leu Lys Lys Ser Glu Lys Ile Leu Asn

[illegible]

175					180					185					190	
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Leu	Asp	Arg	Ile	Asn	Ser	Ser	Asn	Asp	Ile	Asp	Phe	Lys	Leu	Ile	Asn	
				195					200					205		
tgt	acc	gac	acc	acc	aag	ttc	gtc	tgg	atc	aag	gac	ttc	aac	atc	ttc	675
Cys	Thr	Asp	Thr	Thr	Lys	Phe	Val	Trp	Ile	Lys	Asp	Phe	Asn	Ile	Phe	
			210					215					220			
ggg	cgt	gag	ctg	aac	gcc	acc	gag	gtc	tcc	tcc	ctg	tac	tgg	atc	cag	723
Gly	Arg	Glu	Leu	Asn	Ala	Thr	Glu	Val	Ser	Ser	Leu	Tyr	Trp	Ile	Gln	
		225					230					235				
tcc	tcc	acc	aac	acc	ctg	aag	gac	ttc	tgg	gga	aac	cca	ctg	cgt	tac	771
Ser	Ser	Thr	Asn	Thr	Leu	Lys	Asp	Phe	Trp	Gly	Asn	Pro	Leu	Arg	Tyr	
	240					245					250					
gac	acc	cag	tac	tac	ctg	ttc	aac	cag	ggg	atg	cag	aac	atc	tac	atc	819
Asp	Thr	Gln	Tyr	Tyr	Leu	Phe	Asn	Gln	Gly	Met	Gln	Asn	Ile	Tyr	Ile	
255					260				265					270		
aag	tac	ttc	tcc	aag	gcc	tcc	atg	ggg	gag	acc	gcc	cct	cgt	acc	aac	867
Lys	Tyr	Phe	Ser	Lys	Ala	Ser	Met	Gly	Glu	Thr	Ala	Pro	Arg	Thr	Asn	
				275				280						285		
ttc	aac	aac	gcc	gcc	atc	aac	tac	cag	aac	ctg	tac	ctg	ggg	ctg	cgt	915
Phe	Asn	Asn	Ala	Ala	Ile	Asn	Tyr	Gln	Asn	Leu	Tyr	Leu	Gly	Leu	Arg	
			290					295					300			
ttc	atc	atc	aag	aag	gcc	tcc	aac	tcc	cgt	aac	atc	aac	aac	gac	aac	963
Phe	Ile	Ile	Lys	Lys	Ala	Ser	Asn	Ser	Arg	Asn	Ile	Asn	Asn	Asp	Asn	
		305					310					315				
atc	gtc	cgt	gag	ggg	gac	tac	atc	tac	ctg	aac	atc	gac	aac	atc	tcc	1011
Ile	Val	Arg	Glu	Gly	Asp	Tyr	Ile	Tyr	Leu	Asn	Ile	Asp	Asn	Ile	Ser	
	320					325					330					
gac	gag	tcc	tac	cgt	gtc	tac	gtc	ctg	gtc	aac	tcc	aag	gag	atc	cag	1059
Asp	Glu	Ser	Tyr	Arg	Val	Tyr	Val	Leu	Val	Asn	Ser	Lys	Glu	Ile	Gln	
335					340					345				350		
acc	cag	ctg	ttc	ctg	gcc	cca	atc	aac	gac	gac	cct	acc	ttc	tac	gac	1107
Thr	Gln	Leu	Phe	Leu	Ala	Pro	Ile	Asn	Asp	Asp	Pro	Thr	Phe	Tyr	Asp	
				355					360					365		
gtc	ctg	cag	atc	aag	aag	tac	tac	gag	aag	acc	acc	tac	aac	tgt	cag	1155
Val	Leu	Gln	Ile	Lys	Lys	Tyr	Tyr	Glu	Lys	Thr	Thr	Tyr	Asn	Cys	Gln	
			370					375					380			
atc	ctg	tgc	gag	aag	gac	acc	aag	acc	ttc	gga	ctg	ttc	ggg	atc	ggg	1203
Ile	Leu	Cys	Glu	Lys	Asp	Thr	Lys	Thr	Phe	Gly	Leu	Phe	Gly	Ile	Gly	
		385					390					395				
aag	ttc	gtc	aag	gac	tac	ggg	tac	gtc	tgg	gac	acc	tac	gac	aac	tac	1251
Lys	Phe	Val	Lys	Asp	Tyr	Gly	Tyr	Val	Trp	Asp	Thr	Tyr	Asp	Asn	Tyr	
	400					405					410					
ttc	tgt	atc	tcc	cag	tgg	tac	ctg	cgt	cgt	atc	tcc	gag	aac	atc	aac	1299
Phe	Cys	Ile	Ser	Gln	Trp	Tyr	Leu	Arg	Arg	Ile	Ser	Glu	Asn	Ile	Asn	
415					420					425					430	

Ser	Tyr	Arg	Val	Tyr	Val	Leu	Val	Asn	Ser	Lys	Glu	Ile	Gln	Thr	Gln	
			340					345					350			
Leu	Phe	Leu	Ala	Pro	Ile	Asn	Asp	Asp	Pro	Thr	Phe	Tyr	Asp	Val	Leu	
		355					360					365				
Gln	Ile	Lys	Lys	Tyr	Tyr	Glu	Lys	Thr	Thr	Tyr	Asn	Cys	Gln	Ile	Leu	
	370					375					380					
Cys	Glu	Lys	Asp	Thr	Lys	Thr	Phe	Gly	Leu	Phe	Gly	Ile	Gly	Lys	Phe	
385					390					395					400	
Val	Lys	Asp	Tyr	Gly	Tyr	Val	Trp	Asp	Thr	Tyr	Asp	Asn	Tyr	Phe	Cys	
				405					410					415		
Ile	Ser	Gln	Trp	Tyr	Leu	Arg	Arg	Ile	Ser	Glu	Asn	Ile	Asn	Lys	Leu	
		420						425					430			
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Glu																

<210> 19
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 <212> DNA
 <213> Artificial Sequence

<220>
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 <221> CDS
 <222> (1)...(1239)

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1				5					10					15		
ttc tcc ccg tct gaa gac aac ttc act aac gac ctg aac aaa ggc gaa																96
Phe	Ser	Pro		Glu	Asp	Asn	Phe	Thr	Asn	Asp	Leu	Asn	Lys	Gly	Glu	
			20					25					30			
gaa atc acc tcc gac act aac atc gaa gct gct gaa gaa aac atc tct																144
Glu	Ile	Thr	Ser	Asp	Thr	Asn	Ile	Glu	Ala	Ala	Glu	Glu	Asn	Ile	Ser	
			35				40					45				
ctg gac ctg atc cag cag tac tac ctg act ttc aac ttc gac aac gaa																192
Leu	Asp	Leu	Ile	Gln	Gln	Tyr	Thr	Leu	Thr	Phe	Asn	Phe	Asp	Asn	Glu	
			50			55					60					
ccg gaa aac atc tcc atc gaa aac ctg tct tcc gac atc atc ggt cag																240
Pro	Glu	Asn	Ile	Ser	Ile	Glu	Asn	Leu	Ser	Ser	Asp	Ile	Ile	Gly	Gln	
			65			70				75					80	
ctg gaa ctg atg ccg aac atc gaa cgc ttc ccg aac ggc aag aaa tac																288
Leu	Glu	Leu	Met	Pro	Asn	Ile	Glu	Arg	Phe	Pro	Asn	Gly	Lys	Lys	Tyr	
				85				90					95			
gaa ctg gac aaa tac acc atg ttc cac tac ctg cgt gct cag gaa ttc																336
Glu	Leu	Asp	Lys	Tyr	Thr	Met	Phe	His	Tyr	Leu	Arg	Ala	Gln	Glu	Phe	
			100					105					110			
gaa cac ggt aaa tct cgt atc gct ctg act aac tcc gtt aac gaa gct																384
Glu	His	Gly	Lys	Ser	Arg	Ile	Ala	Leu	Thr	Asn	Ser	Val	Asn	Glu	Ala	
			115				120						125			

ctg	ctg	aac	ccg	tct	cgc	gtt	tac	acc	ttc	ttc	tct	tcc	gac	tac	gtt	432
Leu	Leu	Asn	Pro	Ser	Arg	Val	Tyr	Thr	Phe	Phe	Ser	Ser	Asp	Tyr	Val	
	130					135					140					
aag	aaa	gtt	aac	aaa	gct	act	gaa	gct	gct	atg	ttc	ctg	ggg	tgg	gtt	480
Lys	Lys	Val	Asn	Lys	Ala	Thr	Glu	Ala	Ala	Met	Phe	Leu	Gly	Trp	Val	
	145				150					155					160	
gaa	cag	ctg	gtt	tac	gac	ttc	acc	gac	gaa	act	tct	gaa	gtt	tcc	acc	528
Glu	Gln	Leu	Val	Tyr	Asp	Phe	Thr	Asp	Glu	Thr	Ser	Glu	Val	Ser	Thr	
				165					170					175		
act	gac	aaa	atc	gct	gac	atc	act	atc	atc	atc	ccg	tac	atc	ggc	ccg	576
Thr	Asp	Lys	Ile	Ala	Asp	Ile	Thr	Ile	Ile	Ile	Pro	Tyr	Ile	Gly	Pro	
			180					185					190			
gct	ctg	aac	atc	ggg	aac	atg	ctg	tac	aaa	gac	gac	ttc	gtt	ggg	gct	624
Ala	Leu	Asn	Ile	Gly	Asn	Met	Leu	Tyr	Lys	Asp	Asp	Phe	Val	Gly	Ala	
		195					200					205				
ctg	atc	ttc	tct	ggc	gct	gtt	atc	ctg	ctg	gaa	ttc	atc	ccg	gaa	atc	672
Leu	Ile	Phe	Ser	Gly	Ala	Val	Ile	Leu	Leu	Glu	Phe	Ile	Pro	Glu	Ile	
	210					215					220					
gct	atc	ccg	gtt	ctg	ggg	acc	ttc	gct	ctg	gtt	tcc	tac	atc	gct	aac	720
Ala	Ile	Pro	Val	Leu	Gly	Thr	Phe	Ala	Leu	Val	Ser	Tyr	Ile	Ala	Asn	
	225				230					235				240		
aaa	gtt	ctg	act	gtt	cag	acc	atc	gac	aac	gct	ctg	tct	aaa	cgt	aac	768
Lys	Val	Leu	Thr	Val	Gln	Thr	Ile	Asp	Asn	Ala	Leu	Ser	Lys	Arg	Asn	
				245					250					255		
gaa	aaa	tgg	gac	gaa	gtt	tac	aaa	tac	atc	gtt	act	aac	tgg	ctg	gct	816
Glu	Lys	Trp	Asp	Glu	Val	Tyr	Lys	Tyr	Ile	Val	Thr	Asn	Trp	Leu	Ala	
			260					265					270			
aaa	gtt	aac	act	cag	atc	gac	ctg	atc	cgt	aag	aag	atg	aaa	gaa	gct	864
Lys	Val	Asn	Thr	Gln	Ile	Asp	Leu	Ile	Arg	Lys	Lys	Met	Lys	Glu	Ala	
		275					280					285				
ctg	gaa	aac	cag	gct	gaa	gct	act	aaa	gct	atc	atc	aac	tac	cag	tac	912
Leu	Glu	Asn	Gln	Ala	Glu	Ala	Thr	Lys	Ala	Ile	Ile	Asn	Tyr	Gln	Tyr	
	290					295					300					
aac	cag	tac	acc	gaa	gaa	gaa	aag	aac	aac	atc	aac	ttc	aac	atc	gat	960
Asn	Gln	Tyr	Thr	Glu	Glu	Glu	Lys	Asn	Asn	Ile	Asn	Phe	Asn	Ile	Asp	
	305				310					315					320	
gac	ctg	tcc	tct	aaa	ctg	aac	gaa	tcc	atc	aac	aaa	gct	atg	atc	aac	1008
Asp	Leu	Ser	Ser	Lys	Leu	Asn	Glu	Ser	Ile	Asn	Lys	Ala	Met	Ile	Asn	
				325				330						335		
atc	aac	aaa	ttc	ctg	aac	cag	tgc	tct	gtt	tcc	tac	ctg	atg	aac	tct	1056
Ile	Asn	Lys	Phe	Leu	Asn	Gln	Cys	Ser	Val	Ser	Tyr	Leu	Met	Asn	Ser	
			340					345					350			
atg	atc	ccg	tac	ggc	gtt	aaa	cgc	ctg	gaa	gac	ttc	gac	gct	tcc	ctg	1104
Met	Ile	Pro	Tyr	Gly	Val	Lys	Arg	Leu	Glu	Asp	Phe	Asp	Ala	Ser	Leu	
		355					360					365				

305		310		315		320
Asp	Leu	Ser	Ser	Lys	Leu	Asn
		325		330		335
Ile	Asn	Lys	Phe	Leu	Asn	Gln
		340		345		350
Met	Ile	Pro	Tyr	Gly	Val	Lys
		355		360		365
Lys	Asp	Ala	Leu	Leu	Lys	Tyr
		370		375		380
Gly	Gln	Val	Asp	Arg	Leu	Lys
		385		390		395
Asp	Ile	Pro	Phe	Gln	Leu	Ser
		405		410		

<210> 21
 <211> 1242
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<221> CDS
 <222> (1)...(1239)

<400> 21	
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Met Ala Pro Gly Ile Cys Ile Asp Val Asn Glu Asp Leu Phe Phe	
1 5 10 15	
atc gct gac aag aac tcc ttc tcc gac gac ttg tcc aag aac gag aga	96
Ile Ala Asp Lys Asn Ser Phe Ser Asp Asp Leu Ser Lys Asn Glu Arg	
20 25 30	
atc gag tac aac acc cag tcc aac tac atc gag aac gac ttc cca atc	144
Ile Glu Tyr Asn Thr Gln Ser Asn Tyr Ile Glu Asn Asp Phe Pro Ile	
35 40 45	
aac gag ttg atc ttg gac acc gac ttg atc tcc aag atc gag ttg cca	192
Asn Glu Leu Ile Leu Asp Thr Asp Leu Ile Ser Lys Ile Glu Leu Pro	
50 55 60	
tcc gag aac acc gag tcc ttg act gac ttc aac gtc gac gtc cca gtc	240
Ser Glu Asn Thr Glu Ser Leu Thr Asp Phe Asn Val Asp Val Pro Val	
65 70 75 80	
tac gag aag caa cca gct atc aag aag att ttc acc gac gag aac acc	288
Tyr Glu Lys Gln Pro Ala Ile Lys Lys Ile Phe Thr Asp Glu Asn Thr	
85 90 95	
atc ttc caa tac ctg tac tct cag acc ttc cct ttg gac atc aga gac	336
Ile Phe Gln Tyr Leu Tyr Ser Gln Thr Phe Pro Leu Asp Ile Arg Asp	
100 105 110	
atc tcc ttg acc tct tcc ttc gac gac gcc ctg ctg ttc tcc aac aag	384
Ile Ser Leu Thr Ser Ser Phe Asp Asp Ala Leu Leu Phe Ser Asn Lys	
115 120 125	
gtc tac tcc ttc ttc tcc atg gac tac atc aag act gct aac aag gtc	432
Val Tyr Ser Phe Phe Ser Met Asp Tyr Ile Lys Thr Ala Asn Lys Val	

	130				135				140								
gtc	gag	gcc	ggt	ttg	ttc	gct	ggt	tgg	gtc	aag	cag	atc	gtc	aac	gat	480	
Val	Glu	Ala	Gly	Leu	Phe	Ala	Gly	Trp	Val	Lys	Gln	Ile	Val	Asn	Asp	145 150 155 160	
ttc	gtc	atc	gag	gct	aac	aag	tcc	aac	acc	atg	gac	aag	att	gcc	gac	528	
Phe	Val	Ile	Glu	Ala	Asn	Lys	Ser	Asn	Thr	Met	Asp	Lys	Ile	Ala	Asp	165 170 175	
atc	tcc	ttg	att	gtc	cca	tac	atc	ggt	ttg	gcc	ttg	aac	gtc	ggt	aac	576	
Ile	Ser	Leu	Ile	Val	Pro	Tyr	Ile	Gly	Leu	Ala	Leu	Asn	Val	Gly	Asn	180 185 190	
gag	acc	gcc	aag	ggt	aac	ttc	gag	aac	gct	ttc	gag	atc	gct	ggt	gcc	624	
Glu	Thr	Ala	Lys	Gly	Asn	Phe	Glu	Asn	Ala	Phe	Glu	Ile	Ala	Gly	Ala	195 200 205	
tcc	atc	ttg	ttg	gag	ttc	atc	cca	gag	ttg	ttg	atc	cca	gtc	gtc	ggt	672	
Ser	Ile	Leu	Leu	Glu	Phe	Ile	Pro	Glu	Leu	Leu	Ile	Pro	Val	Val	Gly	210 215 220	
gcc	ttc	ttg	ttg	gag	tcc	tac	atc	gac	aac	aag	aac	aag	atc	atc	aag	720	
Ala	Phe	Leu	Leu	Glu	Ser	Tyr	Ile	Asp	Asn	Lys	Asn	Lys	Ile	Ile	Lys	225 230 235 240	
acc	atc	gac	aac	gct	ttg	acc	aag	aga	aac	gag	aag	tgg	tcc	gac	atg	768	
Thr	Ile	Asp	Asn	Ala	Leu	Thr	Lys	Arg	Asn	Glu	Lys	Trp	Ser	Asp	Met	245 250 255	
tac	ggt	ttg	atc	gtc	gcc	caa	tgg	ttg	tcc	acc	gtc	aac	acc	caa	ttc	816	
Tyr	Gly	Leu	Ile	Val	Ala	Gln	Trp	Leu	Ser	Thr	Val	Asn	Thr	Gln	Phe	260 265 270	
tac	acc	atc	aag	gag	ggt	atg	tac	aag	gcc	ttg	aac	tac	cag	gcc	caa	864	
Tyr	Thr	Ile	Lys	Glu	Gly	Met	Tyr	Lys	Ala	Leu	Asn	Tyr	Gln	Ala	Gln	275 280 285	
gct	ttg	gag	gag	atc	atc	aag	tac	aga	tac	aac	atc	tac	tcc	gag	aag	912	
Ala	Leu	Glu	Glu	Ile	Ile	Lys	Tyr	Arg	Tyr	Asn	Ile	Tyr	Ser	Glu	Lys	290 295 300	
gag	aag	tcc	aac	att	aac	atc	gac	ttc	aac	gac	atc	aac	tcc	aag	ctg	960	
Glu	Lys	Ser	Asn	Ile	Asn	Ile	Asp	Phe	Asn	Asp	Ile	Asn	Ser	Lys	Leu	305 310 315 320	
aac	gag	ggt	att	aac	cag	gcc	atc	gac	aac	atc	aac	aac	ttc	atc	aac	1008	
Asn	Glu	Gly	Ile	Asn	Gln	Ala	Ile	Asp	Asn	Ile	Asn	Asn	Phe	Ile	Asn	325 330 335	
ggt	tgt	tcc	gtc	tcc	tac	ttg	atg	aag	aag	atg	att	cca	ttg	gcc	gtc	1056	
Gly	Cys	Ser	Val	Ser	Tyr	Leu	Met	Lys	Lys	Met	Ile	Pro	Leu	Ala	Val	340 345 350	
gag	aag	ttg	ttg	gac	ttc	gac	aac	acc	ctg	aag	aag	aac	ttg	ttg	aac	1104	
Glu	Lys	Leu	Leu	Asp	Phe	Asp	Asn	Thr	Leu	Lys	Lys	Asn	Leu	Leu	Asn	355 360 365	
tac	atc	gac	gag	aac	aag	ttg	tac	ttg	atc	ggt	tcc	gct	gag	tac	gag	1152	
Tyr	Ile	Asp	Glu	Asn	Lys	Leu	Tyr	Leu	Ile	Gly	Ser	Ala	Glu	Tyr	Glu	370 375 380	

aag tcc aag gtc aac aag tac ttg aag acc atc atg cca ttc gac ttg	1200
Lys Ser Lys Val Asn Lys Tyr Leu Lys Thr Ile Met Pro Phe Asp Leu	
385 390 395 400	

tcc atc tac acc aac gac acc atc ttg atc gag atg ttc taa	1242
Ser Ile Tyr Thr Asn Asp Thr Ile Leu Ile Glu Met Phe	
405 410	

<210> 22
 <211> 413
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 22

Met Ala Pro Gly Ile Cys Ile Asp Val Asp Asn Glu Asp Leu Phe Phe	
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20 25 30	
Ile Glu Tyr Asn Thr Gln Ser Asn Tyr Ile Glu Asn Asp Phe Pro Ile	
35 40 45	
Asn Glu Leu Ile Leu Asp Thr Asp Leu Ile Ser Lys Ile Glu Leu Pro	
50 55 60	
Ser Glu Asn Thr Glu Ser Leu Thr Asp Phe Asn Val Asp Val Pro Val	
65 70 75 80	
Tyr Glu Lys Gln Pro Ala Ile Lys Lys Ile Phe Thr Asp Glu Asn Thr	
85 90 95	
Ile Phe Gln Tyr Leu Tyr Ser Gln Thr Phe Pro Leu Asp Ile Arg Asp	
100 105 110	
Ile Ser Leu Thr Ser Ser Phe Asp Asp Ala Leu Leu Phe Ser Asn Lys	
115 120 125	
Val Tyr Ser Phe Phe Ser Met Asp Tyr Ile Lys Thr Ala Asn Lys Val	
130 135 140	
Val Glu Ala Gly Leu Phe Ala Gly Trp Val Lys Gln Ile Val Asn Asp	
145 150 155 160	
Phe Val Ile Glu Ala Asn Lys Ser Asn Thr Met Asp Lys Ile Ala Asp	
165 170 175	
Ile Ser Leu Ile Val Pro Tyr Ile Gly Leu Ala Leu Asn Val Gly Asn	
180 185 190	
Glu Thr Ala Lys Gly Asn Phe Glu Asn Ala Phe Glu Ile Ala Gly Ala	
195 200 205	
Ser Ile Leu Leu Glu Phe Ile Pro Glu Leu Leu Ile Pro Val Val Gly	
210 215 220	
Ala Phe Leu Leu Glu Ser Tyr Ile Asp Asn Lys Asn Lys Ile Ile Lys	
225 230 235 240	
Thr Ile Asp Asn Ala Leu Thr Lys Arg Asn Glu Lys Trp Ser Asp Met	
245 250 255	
Tyr Gly Leu Ile Val Ala Gln Trp Leu Ser Thr Val Asn Thr Gln Phe	
260 265 270	
Tyr Thr Ile Lys Glu Gly Met Tyr Lys Ala Leu Asn Tyr Gln Ala Gln	
275 280 285	
Ala Leu Glu Glu Ile Ile Lys Tyr Arg Tyr Asn Ile Tyr Ser Glu Lys	
290 295 300	
Glu Lys Ser Asn Ile Asn Ile Asp Phe Asn Asp Ile Asn Ser Lys Leu	
305 310 315 320	
Asn Glu Gly Ile Asn Gln Ala Ile Asp Asn Ile Asn Asn Phe Ile Asn	
325 330 335	

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Gly	Cys	Ser	Val	Ser	Tyr	Leu	Met	Lys	Lys	Met	Ile	Pro	Leu	Ala	Val	
			340					345					350			
Glu	Lys	Leu	Asp	Phe	Asp	Asn	Thr	Leu	Lys	Lys	Asn	Leu	Leu	Asn		
		355				360					365					
Tyr	Ile	Asp	Glu	Asn	Lys	Leu	Tyr	Leu	Ile	Gly	Ser	Ala	Glu	Tyr	Glu	
	370					375					380					
Lys	Ser	Lys	Val	Asn	Lys	Tyr	Leu	Lys	Thr	Ile	Met	Pro	Phe	Asp	Leu	
385				390						395					400	
Ser	Ile	Tyr	Thr	Asn	Asp	Thr	Ile	Leu	Ile	Glu	Met	Phe				
			405					410								

<210> 23
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 <213> Artificial Sequence

<220>
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<221> CDS
 <222> (1)...(1197)

<400> 23																
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Met	Ser	Leu	Tyr	Asn	Lys	Thr	Leu	Asp	Cys	Arg	Glu	Leu	Leu	Val	Lys	
1				5				10					15			
aac act gac ctg cca ttc atc ggt gac atc agt gac gtg aag act gac																96
Asn	Thr	Asp	Leu	Pro	Phe	Ile	Gly	Asp	Ile	Ser	Asp	Val	Lys	Thr	Asp	
			20					25					30			
atc ttc ctg cgt aag gac atc aac gag gag act gag gtg atc tac tac																144
Ile	Phe	Leu	Arg	Lys	Asp	Ile	Asn	Glu	Glu	Thr	Glu	Val	Ile	Tyr	Tyr	
			35				40					45				
cca gac aac gtg tca gta gac caa gtg atc ctc agt aag aac acc tcc																192
Pro	Asp	Asn	Val	Ser	Val	Asp	Gln	Val	Ile	Leu	Ser	Lys	Asn	Thr	Ser	
			50			55					60					
gag cat gga caa cta gac ctg ctc tac cct agt atc gac agt gag agt																240
Glu	His	Gly	Gln	Leu	Asp	Leu	Leu	Tyr	Pro	Ser	Ile	Asp	Ser	Glu	Ser	
	65				70				75					80		
gag atc ctg cca ggg gag aat caa gtc ttc tac gac aac cgt acc cag																288
Glu	Ile	Leu	Pro	Gly	Glu	Asn	Gln	Val	Phe	Tyr	Asp	Asn	Arg	Thr	Gln	
				85				90						95		
aac gtg gac tac ctg aac tcc tac tac tac cta gag tct cag aag ctg																336
Asn	Val	Asp	Tyr	Leu	Asn	Ser	Tyr	Tyr	Tyr	Leu	Glu	Ser	Gln	Lys	Leu	
			100					105					110			
agt gac aac gtg gag gac ttc act ttc acg cgt tca atc gag gag gct																384
Ser	Asp	Asn	Val	Glu	Asp	Phe	Thr	Phe	Thr	Arg	Ser	Ile	Glu	Glu	Ala	
		115					120					125				
ctg gac aac agt gca aag gtg tac act tac ttc cct acc ctg gct aac																432
Leu	Asp	Asn	Ser	Ala	Lys	Val	Tyr	Thr	Tyr	Phe	Pro	Thr	Leu	Ala	Asn	
		130				135					140					
aag gtg aat gcc ggt gtg caa ggt ggt ctg ttc ctg atg tgg gca aac																480

385

390

395

taa

1200

<210> 24

<211> 399

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 24

Met	Ser	Leu	Tyr	Asn	Lys	Thr	Leu	Asp	Cys	Arg	Glu	Leu	Leu	Val	Lys
1				5					10					15	
Asn	Thr	Asp	Leu	Pro	Phe	Ile	Gly	Asp	Ile	Ser	Asp	Val	Lys	Thr	Asp
		20					25					30			
Ile	Phe	Leu	Arg	Lys	Asp	Ile	Asn	Glu	Glu	Thr	Glu	Val	Ile	Tyr	Tyr
	35					40					45				
Pro	Asp	Asn	Val	Ser	Val	Asp	Gln	Val	Ile	Leu	Ser	Lys	Asn	Thr	Ser
	50				55					60					
Glu	His	Gly	Gln	Leu	Asp	Leu	Leu	Tyr	Pro	Ser	Ile	Asp	Ser	Glu	Ser
65				70					75					80	
Glu	Ile	Leu	Pro	Gly	Glu	Asn	Gln	Val	Phe	Tyr	Asp	Asn	Arg	Thr	Gln
			85						90				95		
Asn	Val	Asp	Tyr	Leu	Asn	Ser	Tyr	Tyr	Tyr	Leu	Glu	Ser	Gln	Lys	Leu
		100					105					110			
Ser	Asp	Asn	Val	Glu	Asp	Phe	Thr	Phe	Thr	Arg	Ser	Ile	Glu	Glu	Ala
	115						120					125			
Leu	Asp	Asn	Ser	Ala	Lys	Val	Tyr	Thr	Tyr	Phe	Pro	Thr	Leu	Ala	Asn
	130				135					140					
Lys	Val	Asn	Ala	Gly	Val	Gln	Gly	Gly	Leu	Phe	Leu	Met	Trp	Ala	Asn
145				150					155					160	
Asp	Val	Val	Glu	Asp	Phe	Thr	Thr	Asn	Ile	Leu	Arg	Lys	Asp	Thr	Leu
			165					170					175		
Asp	Lys	Ile	Ser	Asp	Val	Ser	Ala	Ile	Ile	Pro	Tyr	Ile	Gly	Pro	Ala
	180						185					190			
Leu	Asn	Ile	Ser	Asn	Ser	Val	Arg	Arg	Gly	Asn	Phe	Thr	Glu	Ala	Phe
	195					200					205				
Ala	Val	Thr	Gly	Val	Thr	Ile	Leu	Leu	Glu	Ala	Phe	Pro	Glu	Phe	Thr
	210				215					220					
Ile	Pro	Ala	Leu	Gly	Ala	Phe	Val	Ile	Tyr	Ser	Lys	Val	Gln	Glu	Arg
225				230					235					240	
Asn	Glu	Ile	Ile	Lys	Thr	Ile	Asp	Asn	Cys	Leu	Glu	Gln	Arg	Ile	Lys
			245					250					255		
Arg	Trp	Lys	Asp	Ser	Tyr	Glu	Trp	Met	Met	Gly	Thr	Trp	Leu	Ser	Arg
	260				265							270			
Ile	Ile	Thr	Gln	Phe	Asn	Asn	Ile	Ser	Tyr	Gln	Met	Tyr	Asp	Ser	Leu
	275				280						285				
Asn	Tyr	Gln	Ala	Gly	Ala	Ile	Lys	Ala	Lys	Ile	Asp	Leu	Glu	Tyr	Lys
	290				295				300						
Lys	Tyr	Ser	Gly	Ser	Asp	Lys	Glu	Asn	Ile	Lys	Ser	Gln	Val	Glu	Asn
305				310				315						320	
Leu	Lys	Asn	Ser	Leu	Asp	Val	Lys	Ile	Ser	Glu	Ala	Met	Asn	Asn	Ile
			325					330					335		
Asn	Lys	Phe	Ile	Arg	Glu	Cys	Ser	Val	Thr	Tyr	Leu	Phe	Lys	Asn	Met
	340				345							350			
Leu	Pro	Lys	Val	Ile	Asp	Glu	Leu	Asn	Glu	Phe	Asp	Arg	Asn	Thr	Lys
	355				360						365				
Ala	Lys	Leu	Ile	Asn	Leu	Ile	Asp	Ser	His	Asn	Ile	Ile	Leu	Val	Gly
	370				375						380				

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Glu Val Asp Lys Leu Lys Ala Lys Val Asn Asn Ser Phe Gln Asn
 385 390 395

<210> 25
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 <212> DNA
 <213> Artificial Sequence

<220>
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<221> CDS
 <222> (1)...(1158)

<400> 25
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 1 5 10 15
 aga ctg cca tac gtt gcc gac aag gac tcc atc tcc cag gag atc ttc 96
 Arg Leu Pro Tyr Val Ala Asp Lys Asp Ser Ile Ser Gln Glu Ile Phe
 20 25 30
 gag aac aag atc atc acc gac gag acc aac gtt caa aac tac tcc gac 144
 Glu Asn Lys Ile Ile Thr Asp Glu Thr Asn Val Gln Asn Tyr Ser Asp
 35 40 45
 aag ttc tct ttg gac gag tcc atc ctg gac ggt cag gtc cca atc aac 192
 Lys Phe Ser Leu Asp Glu Ser Ile Leu Asp Gly Gln Val Pro Ile Asn
 50 55 60
 cca gag atc gtc gac cca ctg ttg cca aac gtc aac atg gag cca ttg 240
 Pro Glu Ile Val Asp Pro Leu Leu Pro Asn Val Asn Met Glu Pro Leu
 65 70 75 80
 aac ttg cca ggt gag gag atc gtc ttc tac gac gac atc acc aag tac 288
 Asn Leu Pro Gly Glu Glu Ile Val Phe Tyr Asp Asp Ile Thr Lys Tyr
 85 90 95
 gtc gac tac ttg aac tcc tac tac tac ttg gag tct caa aag ttg tct 336
 Val Asp Tyr Leu Asn Ser Tyr Tyr Tyr Leu Glu Ser Gln Lys Leu Ser
 100 105 110
 aac aac gtc gag aac atc acc ttg acc acc tcc gtc gag gag gcc ttg 384
 Asn Asn Val Glu Asn Ile Thr Leu Thr Thr Ser Val Glu Glu Ala Leu
 115 120 125
 ggt tac tct aac aag atc tac acc ttc ctg cca tcc ttg gct gag aag 432
 Gly Tyr Ser Asn Lys Ile Tyr Thr Phe Leu Pro Ser Leu Ala Glu Lys
 130 135 140
 gtt aac aag ggt gtt caa gct ggt ttg ttc ctg aac tgg gcc aac gag 480
 Val Asn Lys Gly Val Gln Ala Gly Leu Phe Leu Asn Trp Ala Asn Glu
 145 150 155 160
 gtc gtc gag gac ttc acc acc aac atc atg aag aag gac acc ctg gac 528
 Val Val Glu Asp Phe Thr Thr Asn Ile Met Lys Lys Asp Thr Leu Asp
 165 170 175
 aag atc tcc gac gtc tcc gtc atc atc cca tac atc ggt cca gcc ttg 576

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[illegible]

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<210> 26
<211> 386
<212> PRT
<213> Artificial Sequence
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<220>

<223> Synthetic Construct

<400> 26

Met Ala Asn Ser Arg Asp Asp Ser Thr Cys Ile Lys Val Lys Asn Asn
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Arg Leu Pro Tyr Val Ala Asp Lys Asp Ser Ile Ser Gln Glu Ile Phe
20 25 30
Glu Asn Lys Ile Ile Thr Asp Glu Thr Asn Val Gln Asn Tyr Ser Asp
35 40 45
Lys Phe Ser Leu Asp Glu Ser Ile Leu Asp Gly Gln Val Pro Ile Asn
50 55 60
Pro Glu Ile Val Asp Pro Leu Leu Pro Asn Val Asn Met Glu Pro Leu
65 70 75 80
Asn Leu Pro Gly Glu Glu Ile Val Phe Tyr Asp Asp Ile Thr Lys Tyr
85 90 95
Val Asp Tyr Leu Asn Ser Tyr Tyr Tyr Leu Glu Ser Gln Lys Leu Ser
100 105 110
Asn Asn Val Glu Asn Ile Thr Leu Thr Thr Ser Val Glu Ala Leu
115 120 125
Gly Tyr Ser Asn Lys Ile Tyr Thr Phe Leu Pro Ser Leu Ala Glu Lys
130 135 140
Val Asn Lys Gly Val Gln Ala Gly Leu Phe Leu Asn Trp Ala Asn Glu
145 150 155 160
Val Val Glu Asp Phe Thr Thr Asn Ile Met Lys Lys Asp Thr Leu Asp
165 170 175
Lys Ile Ser Asp Val Ser Val Ile Ile Pro Tyr Ile Gly Pro Ala Leu
180 185 190
Asn Ile Gly Asn Ser Ala Leu Arg Gly Asn Phe Asn Gln Ala Phe Ala
195 200 205
Thr Ala Gly Val Ala Phe Leu Leu Glu Gly Phe Pro Glu Phe Thr Ile
210 215 220
Pro Ala Leu Gly Val Phe Thr Phe Tyr Ser Ser Ile Gln Glu Arg Glu
225 230 235 240
Lys Ile Ile Lys Thr Ile Glu Asn Cys Leu Glu Gln Arg Val Lys Arg
245 250 255
Trp Lys Asp Ser Tyr Gln Trp Met Val Ser Asn Trp Leu Ser Arg Ile
260 265 270
Thr Thr Gln Phe Asn His Ile Asn Tyr Gln Met Tyr Asp Ser Leu Ser
275 280 285
Tyr Gln Ala Asp Ala Ile Lys Ala Lys Ile Asp Leu Glu Tyr Lys Lys
290 295 300
Tyr Ser Gly Ser Asp Lys Glu Asn Ile Lys Ser Gln Val Glu Asn Leu
305 310 315 320
Lys Asn Ser Leu Asp Val Lys Ile Ser Glu Ala Met Asn Asn Ile Asn
325 330 335
Lys Phe Ile Arg Glu Cys Ser Val Thr Tyr Leu Phe Lys Asn Met Leu
340 345 350
Pro Lys Val Ile Asp Glu Leu Asn Lys Phe Asp Leu Arg Thr Lys Thr
355 360 365
Glu Leu Ile Asn Leu Ile Asp Ser His Asn Ile Ile Leu Val Gly Glu
370 375 380
Val Asp
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<210> 27

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1 5 10 15	
tcc gag aac agt tac aac gat gac aac atc aac act cct aag gag att	96
Ser Glu Asn Ser Tyr Asn Asp Asp Asn Ile Asn Thr Pro Lys Glu Ile	
20 25 30	
gac gac acc gtc act tct aac aac aac tac gaa aac gac ctg gac cag	144
Asp Asp Thr Val Thr Ser Asn Asn Asn Tyr Glu Asn Asp Leu Asp Gln	
35 40 45	
gtc atc cta aac ttc aac tcc gag tcc gcc cct ggt ctg tcc gag gag	192
Val Ile Leu Asn Phe Asn Ser Glu Ser Ala Pro Gly Leu Ser Asp Glu	
50 55 60	
aag ctg aac ctg acc atc cag aac gac gct tac atc cca aag tac gac	240
Lys Leu Asn Leu Thr Ile Gln Asn Asp Ala Tyr Ile Pro Lys Tyr Asp	
65 70 75 80	
tcc aac ggt aca tcc gat atc gag cag cat gac gtt aac gag ctt aac	288
Ser Asn Gly Thr Ser Asp Ile Glu Gln His Asp Val Asn Glu Leu Asn	
85 90 95	
gtc ttc ttc tac tta gac gct cag aag gtg ccc gag ggt gag aac aac	336
Val Phe Phe Tyr Leu Asp Ala Gln Lys Val Pro Glu Gly Glu Asn Asn	
100 105 110	
gtc aat ctc acc tct tca att gac aca gcc ttg ttg gag cag cct aag	384
Val Asn Leu Thr Ser Ser Ile Asp Thr Ala Leu Leu Glu Gln Pro Lys	
115 120 125	
atc tac acc ttc ttc tcc tcc gag ttc atc aac aac gtc aac aag cct	432
Ile Tyr Thr Phe Phe Ser Ser Glu Phe Ile Asn Asn Val Asn Lys Pro	
130 135 140	
gtg cag gcc gca ttg ttc gta agc tgg att cag cag gtg tta gta gac	480
Val Gln Ala Ala Leu Phe Val Ser Trp Ile Gln Gln Val Leu Val Asp	
145 150 155 160	
ttc act act gag gct aac cag aag tcc act gtt gac aag atc gct gac	528
Phe Thr Thr Glu Ala Asn Gln Lys Ser Thr Val Asp Lys Ile Ala Asp	
165 170 175	
atc tcc atc gtc gtc cca tac atc ggt ctg gct ctg aac atc ggc aac	576
Ile Ser Ile Val Val Pro Tyr Ile Gly Leu Ala Leu Asn Ile Gly Asn	
180 185 190	
gag gca cag aag ggc aac ttc aag gat gcc ctt gag ttg ttg ggt gcc	624
Glu Ala Gln Lys Gly Asn Phe Lys Asp Ala Leu Glu Leu Leu Gly Ala	
195 200 205	
ggt att ttg ttg gag ttc gaa ccc gag ctg ctg atc cct acc atc ctg	672
Gly Ile Leu Leu Glu Phe Glu Pro Glu Leu Leu Ile Pro Thr Ile Leu	

210	215	220	
gtc ttc acg atc aag tcc ttc ctg ggt tcc tcc gac aac aag aac aag			720
Val Phe Thr Ile Lys Ser Phe Leu Gly Ser Ser Asp Asn Lys Asn Lys			
225	230	235	240
gtc att aag gcc atc aac aac gcc ctg aag gag cgt gac gag aag tgg			768
Val Ile Lys Ala Ile Asn Asn Ala Leu Lys Glu Arg Asp Glu Lys Trp			
	245	250	255
aag gaa gtc tat tcc ttc atc gtc tgc aac tgg atg acc aag atc aac			816
Lys Glu Val Tyr Ser Phe Ile Val Ser Asn Trp Met Thr Lys Ile Asn			
	260	265	270
acc cag ttc aac aag cga aag gag cag atg tac cag gct ctg cag aac			864
Thr Gln Phe Asn Lys Arg Lys Glu Gln Met Tyr Gln Ala Leu Gln Asn			
	275	280	285
cag gtc aac gcc atc aag acc atc atc gag tcc aag tac aac tcc tac			912
Gln Val Asn Ala Ile Lys Thr Ile Ile Glu Ser Lys Tyr Asn Ser Tyr			
	290	295	300
acc ctg gag gag aag aac gag ctt acc aac aag tac gat atc aag cag			960
Thr Leu Glu Glu Lys Asn Glu Leu Thr Asn Lys Tyr Asp Ile Lys Gln			
305	310	315	320
atc gag aac gag ctg aac cag aag gtc tcc atc gcc atg aac aac atc			1008
Ile Glu Asn Glu Leu Asn Gln Lys Val Ser Ile Ala Met Asn Asn Ile			
	325	330	335
gac agg ttc ctg acc gag tcc tcc atc tcc tac ctg atg aag ctc atc			1056
Asp Arg Phe Leu Thr Glu Ser Ser Ile Ser Tyr Leu Met Lys Leu Ile			
	340	345	350
aac gag gtc aag atc aac aag ctg cga gag tac gac gag aat gtc aag			1104
Asn Glu Val Lys Ile Asn Lys Leu Arg Glu Tyr Asp Glu Asn Val Lys			
	355	360	365
acg tac ctg ctg aac tac atc atc cag cac gga tcc atc ctg			1146
Thr Tyr Leu Leu Asn Tyr Ile Ile Gln His Gly Ser Ile Leu			
	370	375	380
taa			1149
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<211> 382			
<212> PRT			
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<223> Synthetic Construct			
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Met Ser Ile Cys Ile Glu Ile Asn Asn Gly Glu Leu Phe Phe Val Ala			
1 5 10 15			
Ser Glu Asn Ser Tyr Asn Asp Asp Asn Ile Asn Thr Pro Lys Glu Ile			
20 25 30			
Asp Asp Thr Val Thr Ser Asn Asn Tyr Glu Asn Asp Leu Asp Gln			
35 40 45			
Val Ile Leu Asn Phe Asn Ser Glu Ser Ala Pro Gly Leu Ser Asp Glu			
50 55 60			

Lys	Leu	Asn	Leu	Thr	Ile	Gln	Asn	Asp	Ala	Tyr	Ile	Pro	Lys	Tyr	Asp
65					70					75					80
Ser	Asn	Gly	Thr	Ser	Asp	Ile	Glu	Gln	His	Asp	Val	Asn	Glu	Leu	Asn
				85					90					95	
Val	Phe	Phe	Tyr	Leu	Asp	Ala	Gln	Lys	Val	Pro	Glu	Gly	Glu	Asn	Asn
			100					105					110		
Val	Asn	Leu	Thr	Ser	Ser	Ile	Asp	Thr	Ala	Leu	Leu	Glu	Gln	Pro	Lys
		115					120					125			
Ile	Tyr	Thr	Phe	Phe	Ser	Ser	Glu	Phe	Ile	Asn	Asn	Val	Asn	Lys	Pro
	130					135					140				
Val	Gln	Ala	Ala	Leu	Phe	Val	Ser	Trp	Ile	Gln	Gln	Val	Leu	Val	Asp
145					150					155					160
Phe	Thr	Thr	Glu	Ala	Asn	Gln	Lys	Ser	Thr	Val	Asp	Lys	Ile	Ala	Asp
				165					170					175	
Ile	Ser	Ile	Val	Val	Pro	Tyr	Ile	Gly	Leu	Ala	Leu	Asn	Ile	Gly	Asn
			180					185					190		
Glu	Ala	Gln	Lys	Gly	Asn	Phe	Lys	Asp	Ala	Leu	Glu	Leu	Leu	Gly	Ala
	195						200					205			
Gly	Ile	Leu	Leu	Glu	Phe	Glu	Pro	Glu	Leu	Leu	Ile	Pro	Thr	Ile	Leu
	210					215					220				
Val	Phe	Thr	Ile	Lys	Ser	Phe	Leu	Gly	Ser	Ser	Asp	Asn	Lys	Asn	Lys
225					230					235					240
Val	Ile	Lys	Ala	Ile	Asn	Asn	Ala	Leu	Lys	Glu	Arg	Asp	Glu	Lys	Trp
				245					250					255	
Lys	Glu	Val	Tyr	Ser	Phe	Ile	Val	Ser	Asn	Trp	Met	Thr	Lys	Ile	Asn
			260					265					270		
Thr	Gln	Phe	Asn	Lys	Arg	Lys	Glu	Gln	Met	Tyr	Gln	Ala	Leu	Gln	Asn
		275					280					285			
Gln	Val	Asn	Ala	Ile	Lys	Thr	Ile	Ile	Glu	Ser	Lys	Tyr	Asn	Ser	Tyr
	290					295					300				
Thr	Leu	Glu	Glu	Lys	Asn	Glu	Leu	Thr	Asn	Lys	Tyr	Asp	Ile	Lys	Gln
305					310					315					320
Ile	Glu	Asn	Glu	Leu	Asn	Gln	Lys	Val	Ser	Ile	Ala	Met	Asn	Asn	Ile
				325					330					335	
Asp	Arg	Phe	Leu	Thr	Glu	Ser	Ser	Ile	Ser	Tyr	Leu	Met	Lys	Leu	Ile
			340					345					350		
Asn	Glu	Val	Lys	Ile	Asn	Lys	Leu	Arg	Glu	Tyr	Asp	Glu	Asn	Val	Lys
		355					360					365			
Thr	Tyr	Leu	Leu	Asn	Tyr	Ile	Ile	Gln	His	Gly	Ser	Ile	Leu		
	370					375					380				

<210> 29
 <211> 1227
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct
 <221> CDS
 <222> (1)...(1224)

<400> 29																
atg	gcc	cca	cca	cgt	ctg	tgt	att	aga	gtc	aac	aac	tca	gaa	tta	ttc	48
Met	Ala	Pro	Pro	Arg	Leu	Cys	Ile	Arg	Val	Asn	Asn	Ser	Glu	Leu	Phe	
1				5					10					15		
ttt	gtc	gct	tcc	gag	tca	agc	tac	aac	gag	aac	gat	att	aac	aca	cct	96
Phe	Val	Ala	Ser	Glu	Ser	Ser	Tyr	Asn	Glu	Asn	Asp	Ile	Asn	Thr	Pro	
			20					25					30			

att aac act caa ttt aac aag aga aag gag caa atg tac cag gct ctg	864
Ile Asn Thr Gln Phe Asn Lys Arg Lys Glu Gln Met Tyr Gln Ala Leu	
275 280 285	
caa aac caa gtc gat gct atc aag act gca att gaa tac aag tac aac	912
Gln Asn Gln Val Asp Ala Ile Lys Thr Ala Ile Glu Tyr Lys Tyr Asn	
290 295 300	
aac tat act tcc gat gag aag aac aga ctt gaa tct gaa tac aat atc	960
Asn Tyr Thr Ser Asp Glu Lys Asn Arg Leu Glu Ser Glu Tyr Asn Ile	
305 310 315 320	
aac aac att gaa gaa gag ttg aac aag aaa gtt tct ttg gct atg aag	1008
Asn Asn Ile Glu Glu Glu Leu Asn Lys Lys Val Ser Leu Ala Met Lys	
325 330 335	
aat atc gaa aga ttt atg acc gaa tcc tct atc tct tac ttg atg aag	1056
Asn Ile Glu Arg Phe Met Thr Glu Ser Ser Ile Ser Tyr Leu Met Lys	
340 345 350	
ttg atc aat gag gcc aag gtt ggt aag ttg aag aag tac gat aac cac	1104
Leu Ile Asn Glu Ala Lys Val Gly Lys Leu Lys Lys Tyr Asp Asn His	
355 360 365	
gtt aag agc gat ctg ctg aac tac att ctc gac cac aga tca atc ctg	1152
Val Lys Ser Asp Leu Leu Asn Tyr Ile Leu Asp His Arg Ser Ile Leu	
370 375 380	
gga gag cag aca aac gag ctg agt gat ttg gtt act tcc act ttg aac	1200
Gly Glu Gln Thr Asn Glu Leu Ser Asp Leu Val Thr Ser Thr Leu Asn	
385 390 395 400	
tcc tcc att cca ttt gag ctt tct taa	1227
Ser Ser Ile Pro Phe Glu Leu Ser	
405	

<210> 30
 <211> 408
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 30
 Met Ala Pro Pro Arg Leu Cys Ile Arg Val Asn Asn Ser Glu Leu Phe
 1 5 10 15
 Phe Val Ala Ser Glu Ser Ser Tyr Asn Glu Asn Asp Ile Asn Thr Pro
 20 25 30
 Lys Glu Ile Asp Asp Thr Thr Asn Leu Asn Asn Tyr Arg Asn Asn
 35 40 45
 Leu Asp Glu Val Ile Leu Asp Tyr Asn Ser Gln Thr Ile Pro Gln Ile
 50 55 60
 Ser Asn Arg Thr Leu Asn Thr Leu Val Gln Asp Asn Ser Tyr Val Pro
 65 70 75 80
 Arg Tyr Asp Ser Asn Gly Thr Ser Glu Ile Glu Glu Tyr Asp Val Val
 85 90 95
 Asp Phe Asn Val Phe Phe Tyr Leu His Ala Gln Lys Val Pro Glu Gly
 100 105 110
 Glu Thr Asn Ile Ser Leu Thr Ser Ser Ile Asp Thr Ala Leu Leu Glu

tta aat aat caa tca caa gca ata gaa aaa ata ata gaa gat caa tat	912
Leu Asn Asn Gln Ser Gln Ala Ile Glu Lys Ile Ile Glu Asp Gln Tyr	
290 295 300	
aat aga tat agt gaa gaa gat aaa atg aat att aac att gat ttt aat	960
Asn Arg Tyr Ser Glu Glu Asp Lys Met Asn Ile Asn Ile Asp Phe Asn	
305 310 315 320	
gat ata gat ttt aaa ctt aat caa agt ata aat tta gca ata aac aat	1008
Asp Ile Asp Phe Lys Leu Asn Gln Ser Ile Asn Leu Ala Ile Asn Asn	
325 330 335	
ata gat gat ttt ata aac caa tgt tct ata tca tat cta atg aat aga	1056
Ile Asp Asp Phe Ile Asn Gln Cys Ser Ile Ser Tyr Leu Met Asn Arg	
340 345 350	
atg att cca tta gct gta aaa aag tta aaa gac ttt gat gat aat ctt	1104
Met Ile Pro Leu Ala Val Lys Lys Leu Lys Asp Phe Asp Asp Asn Leu	
355 360 365	
aag aga gat tta ttg gag tat ata gat aca aat gaa cta tat tta ctt	1152
Lys Arg Asp Leu Leu Glu Tyr Ile Asp Thr Asn Glu Leu Tyr Leu Leu	
370 375 380	
gat gaa gta aat att cta aaa tca aaa gta aat aga cac cta aaa gac	1200
Asp Glu Val Asn Ile Leu Lys Ser Lys Val Asn Arg His Leu Lys Asp	
385 390 395 400	
agt ata cca ttt gat ctt tca cta tat acc taa	1233
Ser Ile Pro Phe Asp Leu Ser Leu Tyr Thr	
405 410	

<210> 32
 <211> 410
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 32
Met Ala Lys Asn Thr Gly Lys Ser Glu Gln Cys Ile Ile Val Asn Asn
1 5 10 15
Glu Asp Leu Phe Phe Ile Ala Asn Lys Asp Ser Phe Ser Lys Asp Leu
20 25 30
Ala Lys Ala Glu Thr Ile Ala Tyr Asn Thr Gln Asn Asn Thr Ile Glu
35 40 45
Asn Asn Phe Ser Ile Asp Gln Leu Ile Leu Asp Asn Asp Leu Ser Ser
50 55 60
Gly Ile Asp Leu Pro Asn Glu Asn Thr Glu Pro Phe Thr Asn Phe Asp
65 70 75 80
Asp Ile Asp Ile Pro Val Tyr Ile Lys Gln Ser Ala Leu Lys Lys Ile
85 90 95
Phe Val Asp Gly Asp Ser Leu Phe Glu Tyr Leu His Ala Gln Thr Phe
100 105 110
Pro Ser Asn Ile Glu Asn Leu Gln Leu Thr Asn Ser Leu Asn Asp Ala
115 120 125
Leu Arg Asn Asn Asn Lys Val Tyr Thr Phe Phe Ser Thr Asn Leu Val
130 135 140

Asp	Cys	Ile	Arg	Asn	Asn	Asn	Ser	Gly	Trp	Lys	Ile	Ser	Leu	Asn	Tyr
		115					120					125			
Asn	Lys	Ile	Ile	Trp	Thr	Leu	Gln	Asp	Thr	Ala	Gly	Asn	Asn	Gln	Lys
	130					135					140				
Leu	Val	Phe	Asn	Tyr	Thr	Gln	Met	Ile	Ser	Ile	Ser	Asp	Tyr	Ile	Asn
145					150					155					160
Lys	Trp	Ile	Phe	Val	Thr	Ile	Thr	Asn	Asn	Arg	Leu	Gly	Asn	Ser	Arg
			165						170					175	
Ile	Tyr	Ile	Asn	Gly	Asn	Leu	Ile	Asp	Glu	Lys	Ser	Ile	Ser	Asn	Leu
		180						185					190		
Gly	Asp	Ile	His	Val	Ser	Asp	Asn	Ile	Leu	Phe	Lys	Ile	Val	Gly	Cys
	195						200					205			
Asn	Asp	Thr	Arg	Tyr	Val	Gly	Ile	Arg	Tyr	Phe	Lys	Val	Phe	Asp	Thr
	210					215					220				
Glu	Leu	Gly	Lys	Thr	Glu	Ile	Glu	Thr	Leu	Tyr	Ser	Asp	Glu	Pro	Asp
225					230					235					240
Pro	Ser	Ile	Leu	Lys	Asp	Phe	Trp	Gly	Asn	Tyr	Leu	Leu	Tyr	Asn	Lys
			245					250						255	
Arg	Tyr	Tyr	Leu	Asn	Leu	Leu	Arg	Thr	Asp	Lys	Ser	Ile	Thr	Gln	
		260					265					270			
Asn	Ser	Asn	Phe	Leu	Asn	Ile	Asn	Gln	Gln	Arg	Gly	Val	Tyr	Gln	Lys
	275						280					285			
Pro	Asn	Ile	Phe	Ser	Asn	Thr	Arg	Leu	Tyr	Thr	Gly	Val	Glu	Val	Ile
	290					295					300				
Ile	Arg	Lys	Asn	Gly	Ser	Thr	Asp	Ile	Ser	Asn	Thr	Asp	Asn	Phe	Val
305				310					315					320	
Arg	Lys	Asn	Asp	Leu	Ala	Tyr	Ile	Asn	Val	Val	Asp	Arg	Asp	Val	Glu
			325					330					335		
Tyr	Arg	Leu	Tyr	Ala	Asp	Ile	Ser	Ile	Ala	Lys	Pro	Glu	Lys	Ile	Ile
		340					345					350			
Lys	Leu	Ile	Arg	Thr	Ser	Asn	Ser	Asn	Asn	Ser	Leu	Gly	Gln	Ile	Ile
	355					360						365			
Val	Met	Asp	Ser	Ile	Gly	Asn	Asn	Cys	Thr	Met	Asn	Phe	Gln	Asn	Asn
	370					375					380				
Asn	Gly	Gly	Asn	Ile	Gly	Leu	Leu	Gly	Phe	His	Ser	Asn	Asn	Leu	Val
385					390				395						400
Ala	Ser	Ser	Trp	Tyr	Tyr	Asn	Asn	Ile	Arg	Lys	Asn	Thr	Ser	Ser	Asn
			405					410				415			
Gly	Cys	Phe	Trp	Ser	Phe	Ile	Ser	Lys	Glu	His	Gly	Trp	Gln	Glu	Asn
			420					425					430		